Program and Abstracts

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Geographical Distribution and Diversity of Plantago Lanceolata Latent Virus, a Member of the Capulavirus Genus

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Abstract

The genus *Capulavirus* is a new genus in the family *Geminiviridae* that contains so far four species (*Alfalfa leaf curl virus*, *Euphorbia caput-medusae latent virus*, *French bean severe leaf curl virus* and *Plantago lanceolata latent virus*) that infect both cultivated and non-cultivated plants. Among them, plantago lanceolata latent virus (PlLV) infects ribwort plantain (*Plantago lanceolata* L.), a perennial herb that is native from Eurasia and is now widespread all over the world. PlLV is transmitted by the aphid *Dysaphis plantaginea*, which has a holocyclic lifestyle with two successive host plants: apple and plantain. Mechanical inoculation of sap using carborundum powder or syringe have also proved effective to infect various plants including *P. lanceolata*. Although plants naturally infected with PlLV displayed yellowing symptoms, agroinoculation in controlled conditions of an agroinfectious clone of PlLV in plantain did not reveal evidence of symptoms. In order to better decipher the prevalence and the diversity of PlLV, *P. lanceolata* plant samples were collected from four European countries (Finland, France, Italy and Spain), as well as from Iran and South Africa, and were tested by PCR for the presence of PlLV. While PlLV was initially reported from the Åland Islands (South-West Finland), we show that PlLV is also found from all sampled countries but South Africa. These results suggest that the geographic distribution of PlLV is larger than initially thought and that PlLV prevalence is probably relatively high in the Old World. Six complete genomes of PlLV from four distinct plant populations [Finland (2 genomes), France (1), Italy (1), Spain (1)] were amplified by RCA and/or PCR using a pair of abutting primers from infected samples, cloned and sequenced (Sanger). Partial nucleotidic sequences of the coat protein (*cp*) and replication-associated protein (*rep*) genes of PlLV were also obtained by PCR from samples collected in France (1) and Iran (2). The six PlLV complete genome sequences ranged in size from 2832 to 2834 nt in length and shared 94.1% genome-wide pairwise identity. The characterization of capulaviruses from wild asymptomatic plants such as PlLV is essential to better understanding the ecology and the evolution of geminiviruses.